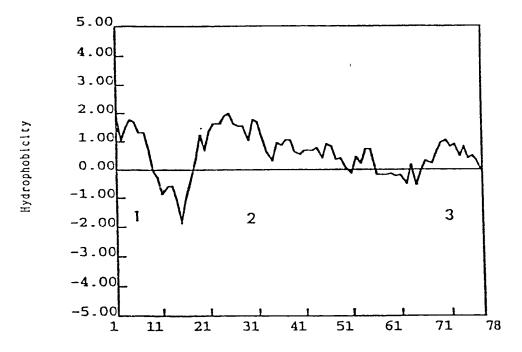
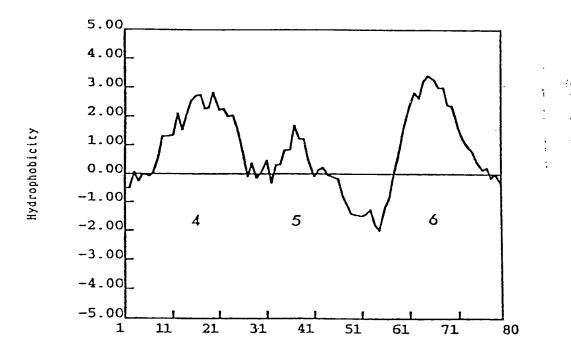
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5.	CLC	œc	ATG	CIG	GCC	λλC	œ	CIG	CIC	TGT	CAT	GTC	ATC	TTC	AAG	AAC	CAG	
									Val	Cys	His	Val	Ile	Phe	Lys	Asn	Gln	Arg
			64			73			82			91			100			109
	ATG	CXC	TCS	CCC.	ACC	ACC	arc	TTC	ATC	CIC	AAC	CIG	GCA	CII	$\alpha \alpha \alpha$	GAC	ATA	АТG
	Met	His	Ser	Ala	Thr	Ser	Leu	Phe	Ile	Val	Asn	Leu	Ala	Val	Ala	Хър	Ile	Met
			118			127						145			154			163
	ATC	ACG	CIG	CIC	AAC	ACC	∞	TTC	ACT	TTG	CIT	α	TTT	GIG	AAC	ACC	ACA	TOG
ν,	Ile	The	Leu	Leu	Asn	The	Pro	Phe	Thr	Leu	Val	Arg	Phe	Val	Asn	Ser	Thr	Trp
			172			181			190			199			208			217
	ATA	TTT	ccc	AAG	œc	ATG	TOC	CAT	GIC	AGC	ccc	TIT	α	CAG	TAC	TGC	TCA	CIG
	Ile	Phe	Gly	Lys	Gly	Met	Cys	His	Val	Ser	Arg	Phe	Ala	Gln	Tyr	СХа	Ser	Leu
			226			235												
	CAC	GIC	TCA	GCA	CIG	ACA	3.											
	Hie	77a 1	Sar	Ala	Leu	The												
		*41																

			9			TO			41			20			43			34
5'	GAG	CCA	CCT	CAC	CIC	TIC	TCG	AAG	AAC	CIG	GAC	TTG	$\alpha\alpha$	ACC	TIC	ATC	CIG	CIC
	Glu	Pro	Ala	Asp	Leu	Phe	طتت	ГУЗ	Asn	Leu	Asp	Leu	Pro	Thr	Phe	Ile	Leu	Leu
			63			72			81			90			99			108
	AAC	ATC	CIG									TAC						AAA
	Asn	Ile	Leu	Pro	Leu	Leu	Ile	Ile	Ser	Val	Ala	Tyr	Val	Arg	Val	Thr	Lys	Lys
			117			126			135			144			153			162
	CMC	TYY										ACA					CCC	
										313		ACA						
	T						-									Dh -	11-	T
	Leu	Tip	æu	суз	ASII	Mec	TTE	vai	ASD	vaı	inr	Thr	GIU	CIII	ıyr	Pne	ALA	Leu
			171			180			189			198			207			216
`	CCCG	CCC										ATG						TTT
	Arg	Pro	Lys	Lys	Lys	Lys	Thr	Ile	Lys	Met	Leu	Met	Leu	Val	Val	Val	Leu	Phe
						4												
			225															
	CCC	CIC	TGC	TGG	TIG	α	CIC	GAC	3'									
	Ala	Leu	Cys	Trp	Leu	Pro	Leu	Asp										
		-					-											

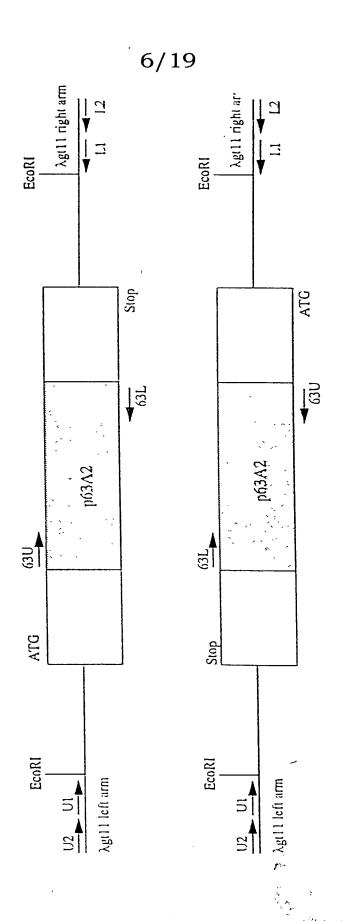


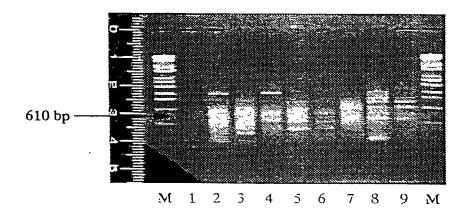
The position in the amino acid sequence



The position in the amino acid sequence

		10	20	30	40	50	
p63A2	1	VCHVIFRNOR!	MHSATSLFIV	NLAVADIMIT	LINTPFTLVR	EVNSTVIEGK	50
P30731	1	ACHAILENVOS	MHSATSLFIV	NLAVADIĤIT	LLNTESTLVR	EVNST VFCK	50
		60	70	80	90	100	
p63A2	51	GMCHVSRFAQ		30	20	100	100
P30731	51	GMCHYSRE 30	YCSLHVSALT	LTALAVDRHQ	VIMHPLKPRI	SITKGVIYLA	100
		110	120	130	. 140	150	
p63A2	101	120	120	130	EP.	ADLEWKNLDL	150
P30731	101	VIWVMATFFS	LPHAICQKLF	TFKYSEDIVR	SICLPDFPER	ADLEWKYLDL	150
`							
		160	170	180	190	200	
p63A2	151	PIFILINILE	LLIISVAYVR	VIKKLWLCNM	ŢVĎVŢŢĒQYF	ALRPKKKKTI	200
P30731	151	PTFILLYLLS ATFILLYLLS	LFILSVAYAR	VAKKLITICNT	ICDALLEGAL	<u>ALRRKKKTT</u> V	200
		210	220	230	240	250	
o63A2	201	KILMLVVVL.					250
P30731	201	kmivizvizi:					250





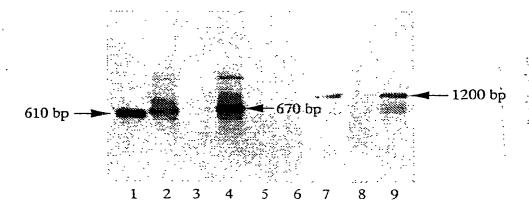
 $M: \; \lambda DNA/Sty \; I \quad \text{marker}$

lane 1; 63U~63L lane 2: U1~63U lane 3; U1~63L lane 4: U2~63U

lane 5; U2~63L

lane 6: L1~63U lane 7: L1~63L

lane 8; L2~63U lane 9; L2~63L

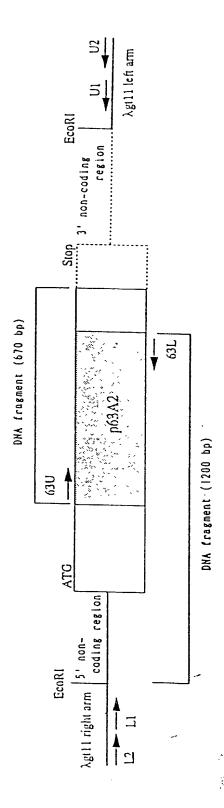


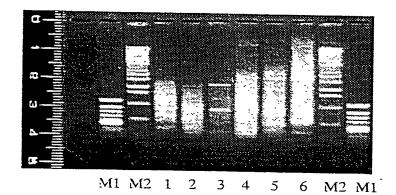
lane 1; 63U~63L lane 2; U1~63U lane 3; U1~63L lane 4; U2~63U lane 5; U2~63L lane 6; L1~63U lane 7; L1~63L lane 8; L2~63U

lane 9; L2~63L

MUSGIR. DNA	63A2-5'. SEQ	MUSGIR. DNA	63A2-5". SEQ	MUSGIR. DNA	63A2-5'. SEQ	MUSGIR. DNA	63A2-5". SEQ	MUSGIR. DNA	63A2-5'. SEQ	MUSGIR. DNA	63.42-5°. SEQ	MUSGIR. DNA	63.42-5". SEQ
### ##################################	360 370 380 CAGAACCCCACGGTGAAAGCCCTGCTC	AACTACACTTTCTCTGACTGGCAGAACTTCGTGGGCAGAGACGTTATGGGGCCGAGTCC 420 430 440 450 460 470	300 310 320 330 340 350 AACTACACCTTCTCCGACTGGCAGAACTTTGTGGGCAGGAGGTGCTACGGCGCTGAGTCC	CATCCCAGCATGGAGGCAGCCTGACCGGGCCCAACGCCTCCTCGCACTTCTGGGCC 360 370 380 390 400 410	240 250 260 270 280 290 GAGCAGAGGGGGAGGGGGCGGGGGGGGGGGGGGGGGGG	CTGCTTCTCTTCTTCTGTGCGAGTACTACTGAGCAACCGCAGGTCGTCACTGAG 300 310 320 330 340 350	250 260 270 280 230 and set of the code of	GCTCAGCCCTTGTGCCTAGAGCTGCAGTGGCT-GGACATGAAGGTTCCTCCTGTC	120 130 140 150 160 170 TTCCTGCCCACAAAGTTCTCCCAGGGAAGGGGTGGCTCCTCCAAAAAATGGTCCCTCACCTC	TAGCCCGGTGCGCTCAGCCCCTCGCACC-CAGCCTCCAGGCACAGAGCCCGGCAGGGA	00 100 100 100 100 100 100 100 100 100	: :: : ::::	10 20 30 40 50 GGGCCCCCTTACACCCTTTGTGATTGAGATCCGGGGTTTC-AAGGGGTGC <u>ATGATG</u> AAG

```
10
                         20
                                  30
                                          40
           TTGCCCCTCCYCATCATCTCTGTGGCCTACGCYCGTGTGGCCAARAAACTGTGGCTGTGT,
ORIG-F. SEQ
            CTTCCACTCTTCATTATCTCAGTGGCCTATGCTCGTGTGGCCAAGAAGCTGTGGCTCTGT
MUSGIR. DNA
         1030
                 1040
                         1050
                                 1060
                                         1070
                                                 1080
                 70
                         80
                                  90
                                          100
                                                  110
OR16-F. SEQ
           AATATGATTGGCGATGTGACCACAGAGCAGTACTTTG-CCTKCGGCGCAAAAAGAAGAAG
           AACACCATTGGCGACGTGACCACAGAGCAGTACCTCGCCCTGCGACGCAAGAAGAAGACC
MUSGIR. DNA
         1090
                 1100
                         1110
                                  1120
                                          1130
                                                  1140
         120
                 130
                         140
                                  150
                                          160
                                                  170
           ACCATCAAGATGTTGATGCTGGTGGTAGTCCCCTTTGCCCTCCGCTGGTTCCCCCTCAAC
OR16-F. SEQ
           MUSGIR. DNA
           ACCGTGAAGATGCTGGTGCTTGTGGTAGTCCTCTTTGCCCTCTGCTGGTTCCCTCTAAC
                 1160
         1150
                          1170
                                  1180
                                          1190
                         200
         180
                 190
                                  210
OR16-FASEQ
           TGCTACGTCCTCCTCCTGTCCAGCAAGGTCATCCGC
           ::::: :::::X :
MUSGIR. DNA
           TGCTATGTCCTCCTCTTGTCCAGCAAGGCCATCCAC
         1210
                 1220
                         1230
                                  1240
```





M1; $\phi X174/HincH$

M2; $\lambda/StyI$

lane 1; 63U~Anchor Primer

lane 2: 63-6~Anchor Primer

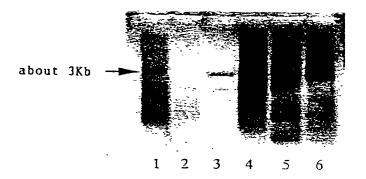
lane 3; 63-7~Anchor Primer

lane 4; 63-6~Anchor Primer lane 5; 63-7~Anchor Primer

lane 6; 63-8~Anchor Primer

Primary PCR

Secondary PCR



lane 1; 63U~Anchor Primer

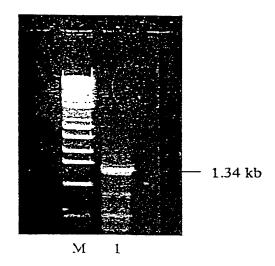
lane 2; 63-6~Anchor Primer

lane 3; 63-7~Anchor Primer lane 4; 63-6~Anchor Primer

lane 5; 63-7~Anchor Primer lane 6; 63-8~Anchor Primer Primary PCR

Secondary PCR

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40
                              30
                       20
          CCCTCTGCTGGTTCCCCCTCAACTGCTACGTCCTCCTCCTGTCCAGCAAGGTCATCCGCA
63A2-3' . sed
          CCCTCTGCTGGTTCCCTCTCAACTGCTATGTCCTCCTCTTGTCCAGCAAGGCCATCCACA
MUSGIR, DNA
                 1200 1210 1220 1230 1240
          CCAACAATGCCCTCTACTTTGCCTTCCACTGGTTTGCCATGAGCAGCACCTGCTATAACC
63A2-3' . seq
          ......
          CCAACAATGCCCTCTACTTTGCCTTCCACTGGTTTGCCATGAGCAGTACTTGTTATAACC
MUSGIR DNA
                                1280
                                       1290
                 1260
                        1270
                                     160
                                            170
                              150
          CCTTCATATACTGCTGGCTGAACGAGAACTYCAGGATTGAGCTAAAGGCATTACTGAGCA
63A2-3' . seq
          CCTTCATCTACTGCTGGCTCAATGAGAACTTTAGGGTTGAGCTTAAGGCATTGCTGAGCA
MUSGIR. DNA
                                       1350
                        1330
                                1340
           1310
                 1320
                                            230
                             210
                                     220
                      200
          63A2-3'. soq
          MUSGIR, DNA
           1370
                                1400
               250
                      260
                              270
                                     280
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63A2-3' . seq
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                                       1470
                 1440
                        1450
                                            350
                                     340
                      320
                              330
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63A2-3'. seq
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MUSGIR. DNA
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                                               1540
                 1500
                        1510
                               1520
           1490
                            390
                                     400
                                               410
                      380
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63A2-3' . seq
                  :::::::
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MUSGIR. DNA
           1550
                                         1590
                                                1600
                          1570
                                 1580
                  1560
mouse GIR stop codon .
                                                 470
                                   450
                                          460
          420
                    430
                          440
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63A2-3'. seq
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             1670
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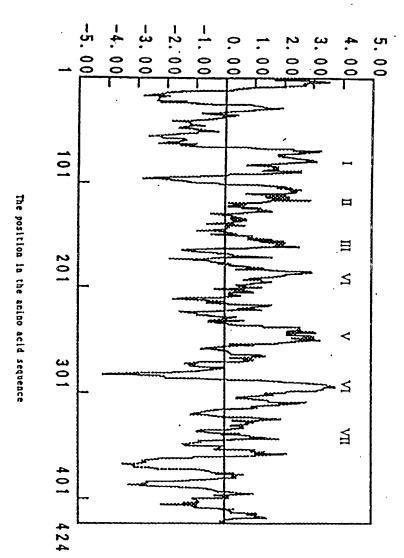
 $M \ ; \ \lambda \, / \, \mathsf{StyI}$ lane 1 ; Whole Brain

18 27 S' ATG GTC CCT CAC CTC TTG CTG CTC TGT CTC CCC TTG GTG CGA GCC ACC GAG Met Val Pre His Leu Leu Leu Cys Leu Leu Pro Leu Val Arg Ala Thr Glu 90 Pro His Glu Gly Arg Ala Asp Glu Gln Ser Ale Glu Ala Ala Leu Ale Val Pro 126 115 144 153 AAT GCC TCG CAC TTC TTC TCT TGG AAC AAC TAC ACC TTC TCC GAC TGG CAG AAC Asn Ala Ser His Phe Phe Ser Trp Asn Asn Tyr Thr Phe Ser Asp Trp Gin Asn 189 198 TIT GTG GGC AGG AGG CGC TAC GGC GCT GAG TCC CAG AAC CCC ACG GTG AAA GCC Phe Val Gly Arg Arg Tyr Gly Ala Glu Ser Gin Asn Pro Thr Val Lys Ala 243 252 CTG CTC ATT GTG GCT TAC TCC TTC ATC ATT GTC TTC TCA CTC TTT GGC AAC GTC Leu Leu Ile Val Ala Tyr Ser Phe Ile Ile Val Phe Ser Leu Phe Gly Asn Val 297 306 CTG GTC TGT CAT GTC ATC TTC AAG AAC CAG CGA ATG CAC TCG GCC ACC AGC CTC Leu Val Cys His Val lie Phe Lys Asn Gln Arg Met His Ser Ale Thr Ser Leu 342 351 360 369 TTC ATC GTC AAC CTG GCA GTT GCC GAC ATA ATG ATC ACG CTG CTC AAC ACC CCC Phe lie Vel Asn Leu Ala Val Ala Asp lie Met lie Thr Leu Leu Asn Thr Pro-405 414 TTC ACT TTG GTT CGC TTT GTG AAC AGC ACA TGG ATA TTT GGG AAG GGC ATG TGC Phe Thr Leu Val Arg Phe Val Asn Ser Thr Trp Ite Phe Gly Lys Gly Met Cys 450 459 468 CAT GTC AGC CGC TTT GCC CAG TAC TGC TCA CTG CAC GTC TCA GCA CTG ACA CTG His 'Val Ser Arg Pho Ala Gin Tyr Cys Ser Leu His Yel Ser Ala Leu Thr Leu 504 513 522 ACA GCC ATT GCG GTG GAT CGC CAC CAG GTC ATC ATG CAC CCC TTG AAA CCC CGG The Ala 110 Ala Val Asp Arg His Gln Val 110 Met His Pro Leu Lys Pro Arg ATC TCA ATC ACA AAG GGT GTC ATC TAC ATC GCT GTC ATC TGG ACC ATG GCT ACG ile Ser lie The Lys Gly Val ile Tyr lie Ale Val ile Trp The Mat Ale The 612 621 6 J O TTC TTT TCA CTC CCA CAT GCT ATC TGC CAG AAA TTA TTT ACC TTC AAA TAC AGT Phe Phe Ser Leu Pro His Ala Ile Cys Gln Lys Leu Phe Thr Phe Lys Tyr Ser 666 675 684 693 GAG GAC ATT GTG CGC TCC CTC TGC CTG CCA GAC TTC CCT GAG CCA GCT GAC CTC Glu Asp IIa Val Arg Ser Leu Cys Leu Pro Asp Pha Pro Glu Pro Ala Asp Leu

> ay Tanggan A

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729
TTC TGG AAG TAC CTG GAC TTG GCC ACC TTC ATC CTG CTC TAC ATC CTG CCC CTC
Phe Trp Lys Tyr Lou Asp Lou Ala Thr Phe ile Lau Lou Tyr ile Lou Pro Lou
                                783
                                                        108
                                           792
CTC ATC ATC TCT GTG GCC TAC GCT CGT GTG GCC AAG AAA CTG TGG CTG TGT AAT
Lau II o II o Sor Val Ala Tyr Ala Arg Val Alu Lys Lys Lou Trp Lou Cys Asn
                                837
                                            A L R
ATG ATT GGC GAT GTG ACC ACA GAG CAG TAC TTT GCC CTG CGG CGC AAA AAG AAG
Mot lie Gly Asp Val Thr Thr Glu Gin Tyr Phe Ala Leu Arg Arg Lys Lys Lys
                    882
                                R 9 1
                                            900
                                                        P 0 P
AAG ACC ATC AAG ATG TTG ATG CTG GTG GTA GTC CTC TTT GCC CTC TGC TGG TTC
Lys Thr lie Lys Met Lou Met Leu Yai Vai Leu Phe Ala Lau Cys Trp Phe
                    936
                                945
                                            954
CCC CTC AAC TGC TAC GTC CTC CTC CTG TCC AGC AAG GTC ATC CGC ACC AAC AAT
Pro Lou Asn Cys Tyr Val Lou Lou Sor Ser Lys Val 110 Arg Thr Asn Asn
                                999
                    990
                                          1008
                                                       1017
                                                                  1025
GCC CTC TAC TTT GCC TTC CAC TGG TTT GCC ATG AGC AGC ACC TGC TAT AAC CCC
Ala Lou Tyr Pho Ala Pho His Trp Pho Ala Mot Sor Sor Thr Cys Tyr Asn Pro
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                                           1062
TTC ATA TAC TGC TGG CTG AAC GAG AAC TTC AGG ATT GAG CTA AAG GCA TTA CTG
Phe lle Tyr Cys Trp Leu Asn Glu Asn Phe Arg Ile Glu Leu Lys Ala Leu Leu
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                               1107
                                           1116
                                                       1125
                                                                    1134
AGC ATG TGT CAA AGA CCT CCC AAG CCT CAG GAG GAC AGG CCA CCC TCC CCA GTT
Ser Met Cys Gin Arg Pro Pro Lys Pro Gin Giu Asp Arg Pro Pro Ser Pro Val
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                                           1170
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Pro Ser Phe Arg Val Ale Trp Thr Glu Lys Asn Asp Gly Gln Arg Ale Pro Leu
                                        1224
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                   1206
                               1215
                                                       1233
                                                                    1242
GCC AAT AAC CTC CTG CCC ACC TCC CAA CTC CAG TCT GGG AAG ACA GAC CTG TCA
Ala Asn Asn Lou Lou Pro Thr Ser Gin Lou Gin Ser Gly Lys Thr Asp Lou Ser
                    1260
TCT GTG GAA CCC ATT GTG ACG ATG AGT TAG 3'
Ser Val Glu Pro ile Val Thr Hat Ser ***
```

Hydrophoblcity



63A2. ANI V Nusgir. Ani	63A2. ANI Nusgir. Ani	63Å2. ÅNI Musgir. Åni	63Å2. ÅMI Musgir. Åmi	63A2. AHI Musgir. Ami	63A2. AMI MUSGIR. AMI	63Å2. ANI Wusgir. Ani	63A2. ANI Musgir. Ani	63A2. AMI Musgir. Ami
00	4 4 5 5		251 251	201 201	55	01	<u> 5 5 </u>	
110 110 (1038) 110 (1038)	360 ENFRIELKAL ENFRVELKAL	10 LFALCWFPLN LFALCWFPLN	260 LPELITSVAY LPL=TISVAY	210 FSLPHAICOK FSLPHAICOK	AOYCSLHVSA AOYCSLHVSA	ORWHSATSLF ORWHSATSLF	60 SDWONFVGRA SDWONFVGRA	
470 KTOLSSVEP KTOLSSVEP	LSMCQRPPKP LSMCQRPPKP	CYVLLLSSK4	27 0 ARVAKKLWLO ARVAKKLWLO	220 LFTFKYSEDI LFTFKYSEDI	170 LTLTAIAVOR LTLTAIAVOR	120 I VNLAVADI N I VNLAVADI N	70 RYGAESQNPT RYGAESQNPT	10-LVRATE
	OEDR-PSPVP OEDR-PSPVP	RINNALYFA HINNALYFA	28 QMIGOVITE NTIGOVITE	VASLCLPDFP VASLCLPDFP	HOVI WHELKP	TILLNIPFIL	VKALLIVAYS VKALLIVAYS	HEGRADEOSA POVVTEHPSA
440	390 SFRVAWTEKY SFRVAWTEKS	HWFAMSSTC FHWFAMSSTC	TALBRKKKK TALBRKKKK	240 EPADLFWKYL EPADLFWKYL	HISTIKGVIV BISTIKGVIV	VRFVNSTW/F	GL LALESTERN BLOWESTER	EAALTGPNAS
450	400 ውርታዊልዎ ተላያነ ዛር ተያለያተ	ANDE I ACATU ANDE I ACATU ANDE I ACATU	THE CANADA SOO	0LATFILLY	200 JAVIWIWATE JAVIWAWATE	GKGMCHVSRF GKGMCHVSRF	ATACHA1 EKS ATACHA1 EKS ATACHA1 EKS	SO EVATA A CANAS SHE SONOTIE
450	4 0 0 0	150 350	3000	250 250	200 200	150	100	5 O